

CC drugs, radiation or cancer), to control expression of heterologous
CC genes placed under control of an Ikaros-responsive element, to
CC treat nervous system diseases (e.g. Alzheimer's disease) and to
CC modulate cell division, amplification or differentiation, especially
CC in haematopoietic cells. Some Ikaros isoforms are antagonistic of
CC others and may be used to inhibit interaction with DNA sequences.
XX
SQ

Sequence 516 AA;

alignment_scores:

Quality: 2750.00 Length: 516
Ratio: 5.329 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-711-417c-165 x AAW70971 ..

Align seg 1/1 to: AAW70971 from: 1 to: 516

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1 MetaspAlaAspGluGlnAspMetSerPheSerSerGlyLysGluSe 17
51 CCCCCCTGTAAGCGTACTCCAGATGAGGGCGATGAGCCCATGCCGATCC 100
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17 rProValSerAspThrProAspGluGlyAspGluProMetProIleP 34
101 CCGAGCACCTCTCCACCACCTCGGGAGGACAGCAAGACTCCAGAGTGAC 150
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34 roGluAspLeuSerThrThrSerGlyGlyGlnGlnSerSerLysSerAsp 50
151 AGAGTCCTGGCCAGTAAATGTAAGTAGAGACTCAGAGTGATGAAGAGAA 200
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51 ArgValValAlaSerAsnValLysValGluThrGlnSerAspGluAs 67
201 TGGGCGTCTGTGAATGAATGGGGAAGAATGTGCGGAGATTACGAA 250
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67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArg 84
251 TGCTTCATGCTCGGAGAGAAATCAATGGCTCCACAGGGACCAAGGC 300
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84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301 AGCTCGCTTTGTGGAGTTGGAGCATTCGACTTCCTAACGGAAAACT 350
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101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTGTATATCTGGGATCATTTTGCATCGGGCCCAATGTCTCATGG 400
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117 uLysCysAspIleCysGlyIleIleCysIleGlyProAsnValLeuMetv 134
401 TTCACAAAAGAACCCACTGGAGAACGGCCCTCCAGTGCAATCAGTGC 450
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134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnCys 150
451 GGGCCCTCATTCACCAAGAGGCAACCTGCTCCGGCACATCAAGCTGCA 500
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151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
501 TTCGGGGAGAACCCCTTCAAATGCCACCTCTGCAACTAGCGCTCGGCC 550
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651 GGAAACATAAAGACGCTGCCACAACTACTTTGGAAAGCATGGGCTTCCGG 700
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701 GCACACTGTACCCAGTCATTAAAGAAGAACTAAGCACAGTGAATGGCA 750
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234 lyThrLeuTyrProValIleLysGluGluThrLysHisSerGluMetAla 250
751 GAAGACCTGTGCAAGATAGATCAGAGATCTCTCGTGTGGACAGACT 800
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251 GluAspLeuCysLysIleGlySerGluArgSerLeuValLeuAspArgLe 267
801 AGCAAGTATATGCGCCAAACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
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1101 CGTGGAGTACCTGCTGCTCTCCAGGCCAAGTTGGTGGCTCCCTCGAGC 1150
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384 rgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGluSer 400
1201 ACAACGAGGAGCAGCGCGCTCTTACTACTGACCAACCAACCATCGC 1250
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1251 CCGACCGCGCACGCGTGTGCTCAAGGAGGAGCAGCGCGCTACGACC 1300
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417 aArgArgAlaGlnArgValSerLeuLysGluGluHisArgAlaTyrAspL 434
1301 TGCTGCGCGCGCTCCGAGAACTCGCAGACGCGCTCCCGGTGGTCAGC 1350
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434 euLeuArgAlaAlaSerGluAsnSerGlnAspAlaLeuArgValValSer 450
1351 ACCAGCGGGAGCAGATGAAGTGTACAAGTGCAGACACTGCCCGGTGCT 1400
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467 uPheLeuAspPheHisValMetTyrThrIleHisMetGlyCysHisGlyPhe 484
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501 GluPheSerSerHisIleThrArgGlyGluHisArgPheHisMetSer 516
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seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT: AAB42333

seq_documentation_block:

ID AAB42333 standard; Protein: 519 AA.

AC AAB42333;

XX DT 08-FEB-2001 (first entry)

XX DE Human ORFX ORF2097 polypeptide sequence SEQ ID NO:4194.

XX KW Human: open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antidiabetic;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antinaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

XX OS Homo sapiens.

XX FN W0200058473-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US08621.

XX PR 31-MAR-1999; 99US-0127607.

XX PR 02-APR-1999; 99US-0127636.

XX PR 05-APR-1999; 99US-0127728.

XX PR 30-MAR-2000; 2000US-0540763.

XX PA (CURA-) CURAGEN CORP.

XX PI Shinkets RA, Leach M;

XX DR WPI; 2000-602362/57.

XX DR N-PSDB; AAC76542.

XX PT Novel nucleic acids and peptides derived from open reading frame X,

XX PT useful for treating e.g. cancers, proliferative disorders,

XX PS neurodegenerative disorders and cardiovascular disease -

XX PS Claim 11; Page 3390-3391; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antinaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 519 AA;

alignment_scores:

Quality: 2644.50 Length: 519
 Ratio: 5.175 Gaps: 3
 Percent Similarity: 98.459 Percent Identity: 96.724

alignment_block:

US-08-711-417c-165 x AAB42333 ..

Align seg 1/1 to: AAB42333 from: 1 to: 519

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 17 rProProValSerAspThrProAspGluGlyAspGluProMetProileP 34
 101 CCGAGGACCTCTCCACACCTCGGGAGGAGCAGCAAGCTCCAAGAGTGAC 150
 34 roGluAspLeuSerThrThrSerGlyGlyGlnGlnSerSerLysSerasp 50
 151 AGAGTCGTGGCCAGTAAATGTTAAAGTAGACTCAGAGTGTGAAGAGAA 200
 51 ArgValValAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
 201 TGGCGGTGCTGTGAATGGAATGCGGAGGAGGATTTACGAA 250
 67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
 251 TGCTTGATGCTCGGGAGAGAAATGAATGGTCCACAGGACCAAGGC 300
 84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
 301 AGTCGCTGTTGTCGGGAGTTGGAGCATTCGACTTCCTTAACGGAAACT 350
 101 SerSerAlaLeuSerGlyValGlyGlyLeuArgLeuProAsnGlyLysLe 117
 351 AAAGTGTGATATCTGGGATCATTTGATCGGGCCCAATGTGCTCATGG 400
 117 uLysCysAspIleCysGlyIleCysIleGlyProAsnValLeuMetV 134
 401 TTCACAAAAGAGCCACACTGGAGAACCGCCTTCCAGTGAATCAGTGC 450
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 151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisLysLeuH 167
 501 TTCGGGGAGAGCCCTTCAATGCCACTCTGCAACTAGCCTCGCCGCC 550
 167 sSerGlyGluLysProPheLysCysHisLeuLysAsnTyrAlaCysArg 184
 551 GGAGGAGCGCCTCAGTGGCCACCTGAGGAGCGCACTCCGTTGGTAAACCT 600
 184 rGArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200
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 651 GGAACATAAGAGCGCTGCCAACACTACTTTGAAAGCATGGGCTTCCGG 700
 217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 234
 701 GCACACTGTACCCAGTCAATTAAGAGAACTAAGCAGACAGTGAATGGA 750
 234 LyThrLeuTyrProValLysGluGluThrAsnHisSerGluMetAla 250
 751 GAAGACCTGTGAAGATAGATCAGAGATCTCTCGTCTGGACAGACT 800

us-08-711-417c-165.rag

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801 AGCAAGTAATGTCGCAACACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
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267 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 284
851 GGACAAAGGCGCTGCGACACGCCCTACGAC...ASTGCCACGTACGAG 897
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284 LysPheGlyLeuSerAspThrProTyrAspSerSerAlaSerTyrGlu 300
898 AAGGAGACCAATATGATGAAGTCCACGCTGATGGACCAAGCCATCAACA 947
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301 LysGluAsnGluMetMetLysSerHisValMetAspGlnAlaIleAsnAs 317
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334 roProGlyGlySerGluValValProValIleSerProMetTyrGlnLeu 350
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384 erGluArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThr 400
1195 GAGAGCAACACAGGAGCAGCAGCGGCTTATCTACCTGACCAACCA 1244
401 GluSerAsnAsnGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHi 417
1245 CATCGCCGACGCGCGCAACG...GTGCTGCTCAAGGAGGAGCAGCGCG 1291
417 sIleAlaProHisAlaArgAsnGlyLeuSerLeuLysGluGluHisArg 434
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434 latyrAspLeuLeuArgAlaAlaSerGluAsnSerGlnAspAlaLeuArg 450
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1392 CCGGGTCTCTTCTCTGATCAGTCACTGTACACCATCCACATGGGCTGCC 1441
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484 isGlyPheArgAspPropheGluCysAsnMetCysGlyTyrHisSerGln 500
1492 GACCGGTACGAGTTCGTGTCGCACATACGCGAGGGGACCGCTTCCA 1541
501 AspArgTyrGluPheSerSerHisIleThrArgGlyGluHisArgPheHi 517
1542 CATGAGC 1548
517 sMetSer 519

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seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:AA46964

seq_documentation_block:

ID: AAR46964 standard; Protein; 537 AA.

XX AAR46964;

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XX 21-OCT-1994 (first entry)
DT Peptide with Ikaros protein activity.
DE Ikaros; zinc finger; protein; immune disorder; therapy; treatment;
KW corpus striatum; regulatory gene.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Misc-difference 536
FT /note= "Position is encoded by a stop codon in the
FT corresponding nucleotide sequence."
XX WO9406814-A.
PN 31-MAR-1994.
PD 14-SEP-1993; 93WO-US08743.
PF 14-SEP-1992; 92US-0946233.
PR (GEHO ) GEN HOSPITAL CORP.
PA Georgopoulos K;
XX WPI; 1994-118387/14.
XX N-PSDB; AAQ44980.
XX T-cell pathway regulatory gene, Ikaros - encodes family of unique
XX zinc finger proteins, useful for treating immune system disorders
XX Claim 14; Page 44-46; 112pp; English.
XX The Ikaros gene encodes a zinc finger protein which can be used in a
XX therapeutic composition to treat animals with an immune system
XX disorder. It may also be used for assessing whether a subject is at
XX risk for an immune disorder. It is of particular use in treating a
XX disorder of the corpus striatum.
XX Sequence 537 AA;

alignment_scores:
Quality: 2480.00 Length: 487
Ratio: 5.221 Gaps: 2
Percent Similarity: 97.536 Percent Identity: 95.688

alignment_block:
US-08-711-417C-165 x AAR46964 ..

Align seg 1/1 to: AAR46964 from: 1 to: 537

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99 GluAspLeuArgMetLeuAspAlaSerGlyGluLysMetAsnGlySerHi 115
288 CAGGACCAAGGAGCTCGCGTTTGTTCGGAGGTGGAGGACTTCGACTTC 337
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338 CTACCGAAACTAAAGTGTATATGCGGATCATTTGCATCGGCC 387
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149 AsnValLeuMetValHisLysArgSerHisThrGlyGluArgProPheG1 165
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438 GTGCAATCAGTCGGGGCCCTATTACCCAGAGGGCAACCTGTCGCCG 487
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165 nCysAsnGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgH 182
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488 ACATCAAGCTGCATCCGGGAGAGCCCTTCAATGCCACCTCTGCAAC 537
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638 GAACGTCTTTAGAGGAACATAAAGAGCGCTGCCACAACTACTTGGAA 687
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232 rgThrSerLeuGluGluHisLysGluArgCysHisAsnTyrLeuGluSer 248
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688 ATGGGCCCTTCGGGCACACTGTACCCAGTCAATTAAAGAAACTAAAGCA 737
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788 TCCTGGACAGACTAGCAAGTAATGTCGCCAAAGTAAAGAGCTCTATGCGCT 837
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299 GlnLysPheLeuGlyAspLysGlyLeuSerAspThrProTyrAspSerAl 315
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988 GTGACAGCCCGCGGGGCTCCGAGGTGTCGGGTGTCATCAGCCCGAT 1037
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349 ValGlnThrProGlyLysSerGluValValProValIleSerProMe 365
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1038 GTACCACTGTCACAGCGCTCGAGGGCACCCCGCGCTCCACCACTCGG 1087
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449 ArgAlaTyrAspLeuValArgAlaAlaSerGluAsnSerGlnAspAlaPh 465
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1388 ACTGCGGCTGCTCTCTGATCAGCTCATGTCACCATCCACATGGGC 1437
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1538 TCCACATGAGC 1548
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532 heHisMetThr 535

seq_name: /STD1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:AA92015
seq_documentation_block:
ID AA92015 standard; Protein; 461 AA.
XX AC
XX AA92015;
XX DT
XX 09-MAY-1996 (first entry)
XX DE
XX Human Ikaros protein hik-1.
XX KW
KW Ikaros; transgene; transgenic animal; transgenic mouse; hik-1;
KW immunocomprised; immune system disorder; nervous system disorder;
KW animal model.
XX OS
XX Homo sapiens.
XX PN
PN WO9604372-A1.
XX PD
PD 15-FEB-1996.
XX PF
PF 28-JUL-1995; 95WO-US09345.
XX PR
PR 29-JUL-1994; 94US-0283300.
XX PA
PA (GEO ) GEN HOSPITAL CORP.
XX PI
PI Georgopoulos K;
XX PT
PT WPI; 1996-129389/13.
XX DR
DR N-PSDB; AAT16060.
XX PS
PS Transgenic rodent having Ikaros trans-gene (pref. mutated) - is
severely immuno-compromised and can be used as model to determine
effects of treatment for immune and nervous system disorders
Disclosure; Fig 2; 102pp; English.
XX CC
CC An almost full-length cDNA sequence (AAT16060) codes for part
(AAR92015) of the human Ikaros protein, a zinc finger protein that is
a master regulator of haematopoietic differentiation and a major
determinant in lymphocyte specification and development. Different
isoforms (see AAR92014 and AAR92016-19) of mouse Ikaros have also been
isolated. Transgenic animals, pref. mice, having a mutated Ikaros
transgene, esp. a mutation that alters the DNA binding domain of the

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CC Ikaros protein, are used as models to determine the effects of
 CC treatments for immune or nervous system disorders.

XX
 SQ Sequence 461 AA;

alignment_scores:
 Quality: 2467.00 Length: 461
 Ratio: 5.351 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-711-417C-165 x AAR92015 ..

Align seg 1/1 to: AAR92015 from: 1 to: 461

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216 AATGAATGGGGAAGTATGCGGAGGATTTACGAATGCTTGATGCTCGG 265
|||||
17 uMeCAsnGlyGluCysAlaGluAspLeuA-gMetLeuAspAlaSerG 34
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266 GAGAGAAATGAATGGTCCACAGGACCAAGCGAGCTCGGCTTGTCTCG 315
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34 LyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50
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51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy 67
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366 TGGGATCATTTGTCATCGGGCCCAATGTGCTCATGTTTCACAAAGAGCC 415
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67 scGlyIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
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416 ACATCGGAGAACGCCCTTCAGTGCAATCAGTGCAGGCTCATTCACCC 465
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84 IsThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100
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466 CAGAAGGGCAACTGCTCCGCGCACATCAAGTGCATTCCGGGGAGAGCC 515
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516 CTTCAATCCCACTCTGCACTAGCTCGCGCGGAGGAGCCCTCA 565
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866 CCGACACGCCCTAGCACAGTGCACGCTTACGAGAAAGGAGAACGAAATGATG 915

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451 IleThrArgGlyGluHisArgPheHisMetSer 461
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seq_documentation_block:
ID AAW72672 standard; Protein; 461 AA.
XX
AC AAW72672;
XX
DT 14-JAN-1999 (first entry)
XX
DE Human Ikaros.
XX
KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
KW differentiation marker; immune system; corpus striatum; AIDS;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US5824770-A.

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XX PD XX PF XX PR PR PR PR XX PA XX XI XX DR DR XX PT PT XX PS XX CC

20-OCT-1998. 05-JUN-1995; 95US-0465590. 02-MAY-1994; 94US-0238212. 14-SEP-1993; 92US-0946233. 14-SEP-1993; 93US-0121438. 05-JUN-1995; 95US-0121438. 05-JUN-1995; 95US-0465590. (GEOH) GEN HOSPITAL CORP.

Georgopoulos K:

WPI; 1998-582621/49.
N-PSDB; AAV66969.

Ikaros poly:peptide(s) - useful for treating disorders of immune system or corpus striatum

Claim 1; Column 55-58; 111pp; English.

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFkB element, an NFkB binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (e) it inhibits protein-protein interactions of transcriptional complexes formed with naturally occurring Ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-responsive elements and/or naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence represents a specifically claimed human Ikaros protein.

Sequence 461 AA.

alignment scores.

Quality:	2467.00	Length:	461
Ratio:	5.351	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment block.

US-08-711-417C-165 X AAW72672

Align seg 1/1 to: AAW72672 from: 1 to: 461

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366 TGGGATCATTTGTCATCGGGCCCAATGTGCTCATGGTTTCACAAAAGAAGCC 415
67 sGlyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
416 ACACGTGGAGAAGCGCCCTTCACGTGCAATCAGTGCCTGGGGGCGCTCATTCAC 465
84 iStHrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100
466 CAGAAGGGCAACCTGCTCGCGCACATCAAGCTGCATTCCTCGGGGAGAAGCC 515
101 GlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysPr 117
516 CTTCAAATGCCACTCTGCAACTACGCTCGCCGCCCGAGGAGGAGCGCCCTCA 565
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616 TGTGGCCGAGCTATAACACAGCGAAGCTCTTAGAGGACATATAAGAGCG 665
151 CysGlyArgSerTyrlsGlnArgThrSerLeuGluGluHisLysGluAr 167
666 CTGCCCAACTACTCTGGAAGCATGGCGCTCCGGGCGACACTGTACCCAG 715
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866 CGCACAGCGCTACGACAGTCCAGTACGAGAGAGAGAGAGCAATGATG 915
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251 LysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrlsLeu 267
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351 ArgSerGlyLeuIleTyrlsThrAsnHisIleAlaArgArgAlaGluArg 367

PT related products, used to treat e.g. rhinorrhea

134 ИСТОРИЯ НАШЕГО НАРОДА

New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and

616 TGTGCGCCGAGCTATAACAGCGACGCTCTTAGAGGACATAGAGCG 665
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seq_documentation_block:

ID AAR92017 standard; Protein; 518 AA.

XX AAR92017;

XX 09-MAY-1996 (first entry)

XX Murine Ikaros protein mIk-1.

XX Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte;
 KW immunocomprised; immune system disorder; nervous system disorder;
 KW animal model; mIk-1.

XX Mus musculus.

XX Key Location/Qualifiers
 FH 119..140
 FT Domain /label= F1
 FT /note= "zinc finger domain F1"
 FT 147..167
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 FT 491..513
 FT Domain /label= F6
 FT /note= "zinc finger domain F6"

XX W09604372-A1.

XX 15-FEB-1996.

XX 28-JUL-1995; 95WO-US09345.

XX 29-JUL-1994; 94US-0283300.

XX (GEO) GEN HOSPITAL CORP.

XX Georgopoulos K;

XX WPI; 1996-129389/13.

XX N-PSDB; T016062.

XX Transgenic rodent having Ikaros trans-gene (pref. mutated) - is
 PT severely immuno-compromised and can be used as model to determine
 PT effects of treatment for immune and nervous system disorders

XX Disclosure; Fig 4; 102pp; English.

XX The sequence of 57.5 kDa mouse Ikaros protein mIk-1 (AAR92017) was
 CC deduced from mouse Ikaros cDNA (AAR16062) isolated from a mature
 CC T-cell line E15 library. Ikaros protein is a master regulator of
 CC hematopoietic differentiation and a major determinant in lymphocyte
 CC differentiation. Other isoforms of Ikaros (see AAR92014, AAR92016 and
 CC AAR92018-19) arise from differential splicing of Ikaros gene
 CC transcripts. transgenic animals, esp. mice, having a mutated Ikaros
 CC transgene, esp. a mutation that alters the DNA binding domain of the
 CC Ikaros protein, are used as models to determine the effects of
 CC treatments for immune or nervous system disorders.

XX

SQ Sequence 518 AA;

alignment_scores:

Quality: 2437.00 Length: 521
Ratio: 4.913 Gaps: 6
Percent Similarity: 95.202 Percent Identity: 89.635

alignment_block:

US-08-711-417c-165 x AAR92017 ..

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34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGACTGCTGGCCGTAATGTTAAAGTAGAGACTCAGAGTCAATGAAGAA 200
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
201 TGGCGCTGCTGTGAATGAATGGGAAGATGTGGGAGGATTTACGAA 250
67 nGlyArgAlaCysGluMetAsnGlyGluGlyCysAlaGluAspLeuArg 84
251 TGCTTGATGCTCGGAGAGAAATGAATGGCTCCACAGGAGGACCAAGGC 300
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgaspGlnGly 100
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101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
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134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer 150
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seq_documentation_block:

ID AAW72674 standard; Protein; 518 AA.

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AC

AAW72674;

XX

DT

14-JAN-1999 (first entry)

XX

DE

Mouse Ikaros mIk-1.

XX

KW

CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS; Alzheimer's disease.

XX

OS

Mus sp.

XX

PN

US5824770-A.

XX

PD

20-OCT-1998.

XX

PF

05-JUN-1995; 95US-0465590.

XX

PR

02-MAY-1994; 94US-0238212.

XX

PR

14-SEP-1992; 92US-0946233.

XX

PR

14-SEP-1993; 93US-0121438.

XX

PR

05-JUN-1995; 95US-0465590.

XX

PA

(GEHO) GEN HOSPITAL CORP.

XX

PI

Georgopoulos K;

XX

DR

WPT; 1998-582621/49.

XX

DR

N-PSDB; AAV66971.

XX

PT

Ikaros poly:peptide(s) - useful for treating disorders of immune system or corpus striatum

XX

PS

Claim 1; Column 61-66; 11pp; English.

XX

CC

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (e) it inhibits protein-protein interactions of transcriptional complexes formed with naturally occurring Ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-responsive elements and/or inhibit protein-protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence represents a specifically claimed mouse Ikaros protein.

XX

SQ Sequence 518 AA;

alignment_scores:

Quality: 2437.00

Length: 521

Ratio: 4.913

Gaps: 6

Percent Similarity: 95.202

Percent Identity: 89.635

alignment_block:

US-08-711-417C-165 x AAW72674 ..

Align seg 1/1 to: AAW72674 from: 1 to: 518

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 601 CACAAATGTGGATATTGTGGCGAAGCTATAACACGCAACGCTCTTTAGA 650
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 217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 234
 701 GCACACTGTACCCAGCTCAATTAAGAGAAACTAAGCACAGTGAATGGCA 750
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ID AAW70966 standard; Protein; 518 AA.
XX
AC AAW70966;
XX
DT 11-JAN-1999 (first entry)
XX
DE Mouse Ikaros isoform mIk-1.
XX
KW Ikaros; mIk-1; transcription factor; mouse; lymphocyte;
KW cell differentiation; T cell; cancer; immunodeficiency;
KW Alzheimer's disease; therapy; diagnosis.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT 119..139
FT /note= "zinc finger motif"

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FT Region 147..167
FT /note= "zinc finger motif"
FT Region 175..195
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XX CA2194256-A.
XX
XX 05-MAR-1998.
XX
XX 02-JAN-1997; 97CA-2194256.
XX
XX 05-SEP-1996; 96US-0711417.
XX
XX (GEO ) GEN HOSPITAL CORP.
XX
XX Georgopoulos K;
XX
XX WPI; 1998-378292/33.
XX
XX N-PSDB; AAV42808.
XX
XX New nucleic acid encoding Ikaros protein involved in early
XX differentiation of lymphocytes - existing in several isoforms, and
XX related products, used to treat e.g. immune diseases or cancer and
XX to control cell differentiation
XX
XX Claim 7; Page 75-77; 158pp; English.
XX
XX This is the amino acid sequence of murine Ikaros protein isoform
XX mIk-1, deduced from a cDNA clone (see AAV42808) obtained from a
XX mature murine T cell line E14 library. Native Ikaros is active
XX in the early stages of lymphocyte differentiation, binding to and
XX activating the CD3-delta gene enhancer (see AAV42804). Proteins
XX of the murine Ikaros family (see also AAW70963 and AAW70965-68) are
XX isoforms that arise from differential splicing of Ikaros gene
XX transcripts, and contain different combinations of zinc fingers.
XX They are expressed primarily in T cells in the adult and may play a
XX role as a genetic switch regulating entry into the T cell lineage.
XX The murine and human sequences (see AAW70964, AAW70969 and AAW70971) are
XX very similar. The invention provides Ikaros nucleic acids, vectors
XX and host cells expressing Ikaros polypeptides. These can be used
XX to treat T and B cell diseases (e.g. immune deficiencies caused by
XX drugs, radiation or cancer), to control expression of heterologous
XX genes placed under control of an Ikaros-responsive element, to
XX treat nervous system diseases (e.g. Alzheimer's disease) and to
XX modulate cell division, amplification or differentiation, especially
XX in haematopoietic cells. Some Ikaros isoforms are antagonistic of
XX others and may be used to inhibit interaction with DNA sequences.
XX
XX Sequence 518 AA;
XX
XX alignment_scores:
XX Quality: 2437.00 Length: 521
XX Ratio: 4.913 Gaps: 6
XX Percent Similarity: 95.202 Percent Identity: 89.635
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seq_documentation_block:

ID AAR46965 standard; Protein; 568 AA.

XX AAR46965;

XX AC

XX	21-OCT-1994 (first entry)
XX	Ikaros zinc finger protein isoform IK-1.
XX	Ikaros; zinc finger; protein; immune disorder; therapy; treatment;
XX	corpus striatum; regulatory gene.
XX	Mus musculus.
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XX	Location/Qualifiers
XX	1..53
XX	/label= Exons 1/2.
XX	54..141
XX	/label= Exon 3.
XX	142..247
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 PN W09406814-A.
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 XX 31-MAR-1994.
 XX PD
 XX 14-SEP-1993; 93WO-US08743.
 XX PF
 XX 14-SEP-1992; 92US-0946233.
 XX PR
 XX (GEHO) GEN HOSPITAL CORP.
 XX PA
 XX Georgopoulos K;
 XX PI
 XX WPI; 1994-118387/14.
 XX DR
 XX

XX T-cell pathway regulatory gene, Ikaros - encodes family of unique
 PT zinc finger proteins, useful for treating immune system disorders
 PT
 XX Claim 14; Figure 4; 112pp; English.
 XX

CC The Ikaros gene encodes a zinc finger protein which can be used in a
 CC therapeutic composition to treat animals with an immune system
 CC disorder. It may also be used for assessing whether a subject is at
 CC risk for an immune disorder. It is of particular use in treating a
 CC disorder of the corpus striatum.
 XX
 XX Sequence 568 AA;

SQ

alignment_scores:

Quality: 2422.00 Length: 571
 Ratio: 4.863 Gaps: 7
 Percent Similarity: 87.215 Percent Identity: 82.137

alignment_block:

US-08-711-417C-165 x AAR46965 ..

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 17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
 101 CCGAGGACCTCTCCACCCTCGGGAGGACAGCAAAAGCTCCAGAGTGAC 150
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XX
DT_09-MAY-1996 (first entry)
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DE_Ikaros protein.
XX
KW_Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte;
KW immunocomprised; immune system disorder; nervous system disorder;
KW animal model.
XX
OS Not specified.
XX
FH Key Location/Qualifiers
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XX
XX 28-JUL-1995; 95WO-US09345.
XX
XX 29-JUL-1994; 94US-0283300.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Georgopoulos K;
XX
XX WPI; 1996-129389/13.
XX
XX Transgenic rodent having Ikaros trans-gene (pref. mutated) - is
XX severely immuno-compromised and can be used as model to determine
XX effects of treatment for immune and nervous system disorders
XX
XX Disclosure; Page 75-76; 102pp; English.
XX
XX The sequence of an Ikaros protein (AA92021) is provided in the
XX specification. Ikaros protein is a major regulator of
XX hematopoietic differentiation and a major determinant in lymphocyte
XX differentiation. Isoforms of Ikaros (see AA92014-19) arise from
XX differential splicing of Ikaros gene transcripts. Transgenic animals,
XX pref. mice, having a mutated Ikaros transgene, esp. a mutation that
XX alters the DNA binding domain of the Ikaros protein, are used as
XX

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CC models to determine the effects of treatments for immune or nervous
 XX system disorders.

SQ Sequence 470 AA;

alignment_scores:

Quality: 2207.50 Length: 468
 Ratio: 5.098 Gaps: 3
 Percent Similarity: 92.521 Percent Identity: 90.385

alignment_block:

US-08-711-417c-165 x AAR92021

Align seg 1/1 to: AAR92021 from: 1 to: 470

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160 GCCAGTAATGTTAAAGTAGAGACTCAGAGTGTGATGAAGAGATGGCGGTGC 209
|||||
3 AlaSerAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAl 19
210 CTGTGAATGAATGGGGAAGATGTGGGAGGATTTACGAATGCTTGATG 259
|||||
19 aCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspA 36
260 CCTGGGAGAGAAATGAATGGCTCCACAGGACCAAGGAGCTCGCT 309
|||||
36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
310 TTGTGGGAGTTGGAGGATTCGACTTCCTAACGGAATACTAAAGTGTGA 359
|||||
53 LeuSerGlyValGlyGlyLeuArgLeuProAsnGlyLysLeuLysCysAs 69
360 TATCTGTGGGATCATTTGCAATCGGGGCCCAATGTGCTCATGTTTCAAAA 409
|||||
69 pileCysGlyLeu***CysIleGlyProAsnValLeuMetValHisLysA 86
410 GAAGCCACTGGAAGACGGCCCTCCAGTGCATCAGTACGTCGGGGCTCA 459
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86 rgSerHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
460 TTCACCAAGAGGCAACCTGCTCCGGCACATCAAGCTGATTCCTGGGGA 509
|||||
103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGI 119
510 GAAGCCCTCAATAGCCACTCTGCAACTACGCTCGCGCGGAGGAG 559
|||||
119 uLysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspA 136
560 CCTCACTGGCCACCTGAGGACGCACTCCGCTTGGTAAACCTCAAAATGT 609
|||||
136 laLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCys 152
610 GGATATTGTGGCGAGCTATAACAGCGAAAGCTTTAGAGGAACATAA 659
|||||
153 GlyTyrCysGlyArgSerTyrLysGlnArg***SerLeuGluGluHisly 169
660 AGAGCGCTGCCACAACCTACTTGAAGAGCATGGCCTTCGGGGGACACTGT 709
|||||
169 sGluArgCysHisAsnTyrLeuGlnSerMetGlyLeuProGly***** 186
710 ACCCACTCATTAAGAGAACTAAGACACAGTGAATGGCAGAAGACCTG 759
|||||
186 **ProValIleLysGluGluThr***His**GluMetAlaGluAspLeu 202
760 TGCAAGATAGGATCAGAGAGATCTCTGCTGGGACAGACTAGCAAGTAA 809
|||||
203 CysLysIleGly***GluArgSerLeuValLeuAspArgLeuAlaSerAs 219
810 TGTGCGCAACGTAAGAGCTCTATGCTCAGAAATTTCTTGGGGACAAG 859
|||||
219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
860 GCCTGTCCGACACGCCCTACGACAGTGCACCTACGAGAGAGAGAACGAA 909

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|||||
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286 erGluValValProValIleSerProMetTyrGlnLeuHis***** 302
1057 TCGGAGGACACCCCGGTCTCAACACTCGGCCAGGACAGCCGCTGGA 1106
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303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
1107 GTACCTGCTGCTCTCCCAAGGCCAAGTTGGTGCCTCGGAGCGCGAGG 1156
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319 ***LeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
1157 CGTCCCGGAGCAACAGCTGCCAAGACTCCACGCGACACGAGAGCAACAAC 1206
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336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn*** 352
1207 GAGGAGCAGCGAGCGCTTATCTACCTGACCAACACATCGCCCGCAGG 1256
|||||
353 GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle***** 369
1257 CGCG...CAACGCGTGTGCTCAAGGAGGACGCGCGCTACGACCTGC 1303
|||||
369 *Ala*****LeuLysGluGlu***ArgAlaLys*****L 386
1304 TCGCGCGCGCTCCGAGAACTCGCAGGACGCGCTCCGCGTGTGTGAGCACC 1353
|||||
386 euArgAlaAlaSerGluAsnSerGlnAspAla***ArgValValSerThr 402
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403 SerGlyGluGln***LysValTyrLysCysGluHisCysArgValLeuPh 419
1404 CTGTGATCAGCTCATGTACACCATCCACATG.....GGCTGCCACG 1444
|||||
419 eleuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
1445 GCTTCCGTGATCCTTTGAGTGCACATGTGCGGTACCCAGCCAGGAC 1494
|||||
436 lyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452
1495 CGGTACGAGTTCTGCTCGCACATACGAGGAGGAGGACCGCTTCCACAT 1544
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453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His** 469
1545 GAGC 1548
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469 *Ser 470

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seq_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW72678

seq_documentation_block:

ID AAW72678 standard; Protein; 470 AA.

XX AAW72678;

XX AC

XX DT 14-JAN-1999 (first entry)

XX Ikaros protein general formula.

XX DE

XX CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;

XX KW differentiation marker; immune system; corpus striatum; AIDS;

XX KW Alzheimer's disease.

[illegible]

alignment_scores:

Quality: 2207.50 Length: 468
 Ratio: 5.098 Caps: 3
 Percent Similarity: 92.521 Percent Identity: 90.385

alignment_block:

US-08-711-417C-165 x AAW72678 ..

Align seg 1/1 to: AAW72678 from: 1 to: 470

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19 acysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspA 36
260 CCTCGGAGAGAAATGAATGGCTCCACAGGACCAGGAGCTCGGCT 309
|||||
36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerAla 52
310 TTGTCTGGGATCATTTGCAATCGGCGCCCAATGTGCTCATGTTCCACAAA 409
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69 pilleCysGlyIle***CysIleGlyProAsnValLeuMetValHisLysA 86
410 GAAGCCACACTGGAGAGAGCGCCCTTCCAGTGCATCATAGTCGGGGCTCA 459
|||||
86 rgSerHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
460 TTCACCCAGAGGCAACCTGCTCCGCGACATCAAGCTGCATTCCGGGGA 509
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136 laLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCys 152
610 GGATATTGTGGCCGAAGCTATAACAGCGAACGCTCTTTAGAGGAACATAA 659
|||||
153 GlyTyrCysGlyArgSerTyrLysGlnArg***SerLeuGluGluHisLy 169
660 AGAGCGCTGCCACACTACTTGGAAAGCATGGCCCTCCGGGACACTGT 709
|||||
169 sGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProGly***** 186
710 ACCAGCTCATTAAGAAGAACTAAGCACAGTGAATGGCAGAGACCTG 759
|||||
186 **ProValIleLysGluGluThr***His***GluMetAlaGluAspLeu 202
760 TGCAGATAGGATCAGAGAGATCTCTGCTGCTGGACAGACTAGCAAGTAA 809
|||||
203 CysLysIleGly***GluArgSerLeuValLeuAspArgLeuAlaSerAs 219
810 TGTCTGCCAACGTAAGAGCTCTATGCTCAGAAATTTCTTGGGGACAAGG 859
|||||
219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
860 GCGTGTCCGACAGCGCCCTACGACAGTGGCCACGTACGAGAGGAACGAA 909
|||||
236 **LeuSerAsp***ProTyrAspSerAla***TyrGluLysGlu***** 252
910 ATGATGAAGTCCCGCTGATGGACCAAGCCATCAACAACGCCATCACTA 959
|||||

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253 MetMet***SerHisValMetAsp***AlaIleAsnAsnAlaIleAsnTy 269
960 CTGGGGGCGAGTCCCTCGCCCGCTGTGTGCAGACCCCGCGCGGT 1009
|||||
269 rLeuGlyAlaGluSerLeuArgProLeuValGlnThrProGly***S 286
1010 CCGAGGTGTCCCGGTATCATCAGCCCGATGTACCAGCTGCAC...AGCGC 1056
|||||
286 erGluValValProValIleSerProMetTyrGlnLeuHis***** 302
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|||||
303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
1107 GTACCTGTCTGCTCTCTCCAAAGCCCAAGTTGTGCTCGGAGCGGAGG 1156
|||||
319 ***LeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
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336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn*** 352
1207 GAGGAGCAGCGCGGTCTTATCTACCTGACCAACACCATCGCCCGACG 1256
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353 GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle***** 369
1257 CCG...CAACGGTGTCTGCTCAAGGAGGAGCAGCGCGCTACGACCTGC 1303
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369 *Ala*****LeuLysGluGlu***ArgAlaTyr*****L 386
1304 TCGCGCGCGCTCCGAGAACTCGCAGGACCGCTCCGCTGTGTGCAGCAC 1353
|||||
386 euArgAlaAlaSerGluAsnSerGlnAspAla***ArgValValSerThr 402
1354 AGCGGGGAGCACAAGGTGTACAAAGTGCAGAACACTCGCGGTGCTCTT 1403
|||||
403 SerGlyGluGln***LysValTyrLysCysGluHisCysArgValLeuPh 419
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|||||
419 eLeuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
1445 GCTTCGCTGATCTTTTGTGAGTGCACATGTGCGGTACCAACAGCGGAC 1494
|||||
436 lyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452
1495 CGGTACGAGTTCTGCTCGCACATACCGGAGGAGGAGCAGCGCTTCCACAT 1544
|||||
453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His** 469
1545 GAGC 1548
|||||
469 *Ser 470

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seq_name: /STDs1/gcdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW70970

seq_documentation_block:

ID AAW70970 standard; Protein; 470 AA.

XX AC AAW70970;

XX DT 11-JAN-1999 (first entry)

XX DE Ikaros isoform 1 consensus.

XX KW Ikaros; mik-1; hlk-1; transcription factor; mouse; human;
 KW lymphocyte; cell differentiation; T cell; cancer;
 KW immunodeficiency; Alzheimer's disease; therapy; diagnosis.

XX OS Mus sp.

XX FT Key

XX Misc-difference 1 Location/Qualifiers

CC and B cell diseases (e.g. immune deficiencies caused by drugs,
 CC radiation or cancer), to control expression of heterologous genes
 CC placed under control of an Ikaros-responsive element, to treat
 CC nervous system diseases (e.g. Alzheimer's disease), and to modulate
 CC cell division, amplification or differentiation, especially
 CC in haematopoietic cells. Some Ikaros isoforms are antagonistic of
 CC others and may be used to inhibit interaction with DNA sequences.
 XX

SQ Sequence 470 AA;

alignment_scores:

Quality: 2204.50 Length: 468
 Ratio: 5.091 Gaps: 3
 Percent Similarity: 92.521 Percent Identity: 90.171

alignment_block:

US-08-711-417c-165 x AAW70970 ..

Align seg 1/1 to: AAW70970 from: 1 to: 470

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|||||
3 AlaSerAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAl 19
210 CTGTCAATGATGGGGAAGAAATGTGCGGAGGATTACGAATGCTTGATG 259
|||||
19 aCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspA 36
260 CCTCGGGAGAGAAATGAATGCCTCCACAGGACCAAGCAGCAGCTCGCT 309
|||||
36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
310 TTGTGCGGAGTTGGAGCATTCGACTTCTTAACGGAAAACTAAAGTGTGA 359
|||||
53 LeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAs 69
360 TATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGTTTCACAAA 409
|||||
69 pIleCysGlyIle***CysIleGlyProAsnValLeuMetValHisLysA 86
410 GAAGCCACTTGGAGAACGGCCCTTCCAGTGCATCATAGTCGGGGCTCA 459
|||||
86 rgSerHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
460 TTCACCCAGAAAGGCAACCTGCTCCGGCACAATCAAGCTGATTCGGGGA 509
|||||
103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGI 119
510 GAAGCCCTTCAATGCCACCTCTGCAACTACGCTCGCCCGCGAGGACG 559
|||||
119 uLysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspA 136
560 CCTCTACTGGCCACTGAGGACGCACTCCGTTGGTAAACCTCACAAATGT 609
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136 laLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCys 152
610 GGATATTGTGCGGACGACTATAACAGCGAAGCTCTTTAGAGAAACATAA 659
|||||
153 GlyTyrCysGlyArgSerTyrLysGlnArg***SerLeuGluGluHisLy 169
660 AGAGCGCTGCCACAACCTACTTGGAAAGCATGGCCCTTCGGGGCACACTGT 709
|||||
169 SGlnArgCysHisAsnTyrLeuGluSerMetGlyLeuProGly***** 186
710 ACCAGTCATTAAGAGAAGAACTTAAGCAGCAGTGAATGGCAGAAGACCTG 759
|||||
186 **ProValIleLysGluGluThr***His***GluMetAlaGluAspLeu 202
760 TGCAGATAGGATACAGAGAGACTCTCGTGTGGAGACAGACTAGCAAGTAA 809
|||||
203 CysLysIleGly***GluArgSerLeuValLeuAspArgLeuAlaSerAs 219

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810 TGTGCCCAACGTAAGAGCTCTATGCTCAGAAATTTCTTGGGACAAGG 859
|||||
219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
860 GCCTGTCCGACAGCCCTACGACAGTCCACGTACGAGAGAGAGAACGAA 909
|||||
236 **LeuSerAsp***ProTyrAspSerAla***TyrGluLysGlu***** 252
910 ATGATGAAGTCCACAGTGATGGACCAAGCCATCAACAAGCCATCAACTA 959
|||||
253 MetMet***SerHisValMetAsp***AlaIleAsnAlaIleAsnTy 269
960 CTTGGGGGCGAGTCCCTGCGCCGCTGTGTGCAGACGCCCGCGGGCGGTT 1009
|||||
269 rLeuGlyAlaGluSerLeuArgProLeuValGlnThrProProGly***S 286
1010 CCGAGTGTGTCGCGTCAATCAGCCGATGTACCAGCTGCAC...AGGCGC 1056
|||||
286 erGluValValProValIleSerProMetTyrGlnLeuHis***** 302
1057 TCGGAGGCGACCCGCGCTCCACACCACTCGGCCAGGACAGCGCGTGGA 1106
|||||
303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
1107 GTACCTGCTGCTCTCTCCAAGCCCAAGTTGCTCGCCTCGGAGCGCGAGG 1156
|||||
319 ***LeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
1157 CGTCCCGGAGCAACAGCTCCCAAGACTCCACGGACACCGAGAGCAACAAC 1206
|||||
336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn*** 352
1207 GAGGACGCGCAGCGGCTCTTACTACCTGACCAACACACATCGCCCGCAG 1256
|||||
353 GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle***** 369
1257 CCGC...CAACGCGTGTGCTCAAGGAGGAGCAGCGCGCTACGACCTGC 1303
|||||
369 *Ala*****LeuLysGluGlu***ArgAlaTyr*****L 386
1304 TCGCGCGCGCTCCGAGAACTCGGAGGAGCGCTCCGCGTGTGTACAGACC 1353
|||||
386 euArgAlaAlaSerGluAsnSerGlnAspAla***ArgValValSerThr 402
1354 ACGGGGGAGCAGATGAAGTGTACAAAGTGCGAACACTGCCGGTGTCTCTT 1403
|||||
403 SerGlyGluGln***LysValTyrLysCysGluHisCysArgValLeuPh 419
1404 COTGATCAGCTCATGTACACCATCCACATG.....GGCTGCCACG 1444
|||||
419 eLeuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
1445 GCTTCCGTGATCCTTTTCAGTGCACATGTGCGGTACCAAGCCAGGAC 1494
|||||
436 lPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452
1495 CGGTACGAGTTCCTGCTCGCACATAACGCGAGGAGGACACCGCTTCCACAT 1544
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453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His** 469
1545 GAGC 1548
|||||
469 *Ser 470

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seq_name: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AA1996.DAT: AAR92016

seq_documentation_block:

ID AAR92016 standard; Protein; 432 AA.

XX
 AAR92016;

DT 08-MAY-1996 (first entry)

XX

Murine Ikaros protein mIk-3.

Ikaro: transgene; transgenic animal; transgenic mouse; lymphocyte; immunocompromised; immune system disorder; nervous system disorder; animal model; mIk-3.

Mus musculus.

WO9604372-A1.

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WPI; 1996-129;
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Disclosure; Pa

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T-cell line E.

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differentiation

AAR92017-19)

transcripts.

transgene, esp
Thyrog proteinIkaros protein
treatments for

Treatments for

Sequence 43:

251	TGCTGTGATGCTCGGGAGAGAAAAATGAATGGCTCCCAAGGACCAAGGC	300
84	etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly	100
301	AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCTTAACGGAAAACT	350
101	SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe	117
351	AAAGTGTGATATCTGTGGGATCATTTTGTGCATCGGCGCCCAATGCTCATGG	400
117	ulysCysaspIleCysGlyIleValCysIleGlyProAsnValleuMetV	134
401	TTCAAAAGAAGCCACACTGGAGAAGCGCCTTCCAGTGAATCAGTGC	450
134	alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer	150
451	GGGGCTCATTCACCCAGAAAGGCAACTGCTCGGGACATCAAGCTGCA	500
151	GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi	167
501	TTCCGGGGAGAAAGCCCTTCAATGCCACTCTGCAACTACGCGCTCGCGCC	550
167	sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrlacysArgA	184
551	GGAGGAGCGCCTCACTGGGCCACCTGAGGAGCGCACTCGTGTGGTAAACCT	600
184	rgArgspAlaLeuThrGlyHisLeuArgThrHisSer	196
601	CACAAATGTGATATTGTGGCGGAAGCTATATAACAGCGCAAGCTCTTTAGA	650
196	196
651	GGAACATAAAGAGCGCTGCCACAACACTACTTGGAAAGCATGGCGCTCCGG	700
196	196
701	GCACACTGTACCCAGTCATTAAGAAGAAACTAAGCACAGTGAATGGCA	750
196	196
751	GAAGACCTGTCCAAGATAGGATCAGAGAGATCTCTCTGTGCTGGACAGACT	800
196	196
801	AGCAAGTAATCTGCCAAACGTAAGAGCTCTATGCCTCAGAAAATTTCTTG	850
197G	197
851	GGGACAAAGGCGCTGTCGACACAGCCCTACGACAGTGCACGTCAGTACAGAAG	900
197	LyAspLysCysLeuSerAspMetProTyrlaspSerAlaAsnTyrlGluLys	213
901	GAGAACGNAATGATGAAGTCCCAGCTGATGGACCAAGCCATCAACAAGC	950
214	Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl	229
951	CATCAACTACTCTGGGGCGAGTCCCTCGCGCCGCTGGTGACAGCGCCC	1000
229	alleAsnTyrlLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp	246
1001	CGGGCGGTCCGAGTGGTCCCGGTCTATCAGCCCGATGTACCAAGCTGCAC	1050
246	roGlySerSerGluValValProValIleSerSerMetTyrlGlnLeuHis	262
1051	AGG...CGCTCGGAGGGACCCCGCGCTCCACACACTCGCGCCAGGACAG	1097
263	LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp...	278
1098	CGCGGTGGAGTACCTGCTGCTCTCCAAGGCCAACTGTGTGCGCTCGG	1147
279	AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSer	295
1148	AGCGCGAGGGCGTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACCGAG	1197

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|||||
295 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 311
1198 AGCAACAACGAGGAGGAGCGCGCTCTTACTCTACCTGACCAACACAT 1247
|||||
312 SerAsnAlaGluGlnArgSerGlyLeuIleTyrLeuThrAsnHis11 328
1248 CGCCCGACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCAGCGCGCT 1294
|:|||||:
328 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAlaT 345
1295 AGACCTGTGCGCGCGCTCGAGAACTCGAGGACGCGCTCGCGG 1344
|:|||||:
345 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 361
1345 GTGAGCAGGCGGAGGAGCAGATGAGGTGTACAGTGGCACTGCCG 1394
|||||
362 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysar 378
1395 GTGTCTTCTCTGATCAGTGTATGATACACCATCCACATG.....G 1435
|||||
378 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 395
1436 GTGCGCACGCGCTTCCGTGATPCTTTTGTGAGTGCAACATGTGCGGCTACCA 1485
|||||
395 lCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 411
1486 AGCAGGACGCGGTACGAGTCTCGTCGCACATACGCGAGGCGCACCG 1535
|||||
412 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisar 428
1536 CTCCACATGAGC 1548
|:|||||:
428 gTyrHisLeuSer 432

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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW72673

```

seq_documentation_block:
ID AAW72673 standard; Protein; 432 AA.
XX AC AAW72673;
XX DT 14-JAN-1999 (first entry)
XX DE Mouse Ikaros mIk-3.
XX KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
XX KW differentiation marker; immune system; corpus striatum; AIDS;
XX KW Alzheimer's disease.
XX OS Mus sp.
XX PN US5824770-A.
XX PD 20-OCT-1998.
XX PF 05-JUN-1995; 95US-0465590.
XX PR 02-MAY-1994; 94US-0238212.
XX PR 14-SEP-1992; 92US-0946233.
XX PR 14-SEP-1993; 93US-0121436.
XX PR 05-JUN-1995; 95US-0465590.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PI Georgopoulos K;
XX DR WPI; 1998-582621/49.
XX DR N-PSDB; AAW66970.
XX Ikaros poly(peptide(s) - useful for treating disorders of immune
XX PT system or corpus striatum
XX

```

Claim 1; Column 57-62; 111pp; English.

PS The present invention describes a purified peptide having at least one
XX of the following properties: (a) it stimulates transcription of a DNA
CC sequence under the control of a delta A element, an NFkB element or an
CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of
CC a delta A element, an NFkB element or an Ikaros binding oligonucleotide
CC consensus sequence; (c) it competitively inhibits the binding of a
CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it
CC competitively inhibits Ikaros binding to Ikaros responsive elements; or
CC (e) it inhibits protein-protein interactions of transcriptional complexes
CC formed with naturally occurring Ikaros isoforms. The proteins, provided
CC that they stimulate gene transcription under the control of delta A
CC elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to
CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,
CC competitively inhibit Ikaros binding to Ikaros-binding oligonucleotides,
CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or
CC inhibit protein-protein interactions of transcriptional complexes with
CC naturally occurring Ikaros isoforms, can be used to treat immune system
CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.
CC Alzheimer's disease. The present sequence represents a specifically
XX claimed mouse Ikaros protein.

SQ Sequence 432 AA;

alignment_scores:
Quality: 1963.00 Length: 521
Ratio: 4.776 Gaps: 6
Percent Similarity: 78.887 Percent Identity: 74.280

alignment_block:

US-08-711-417C-165 x AAW72673

Align seg 1/1 to: AAW72673 from: 1 to: 432

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1 ATGATGCTGACGAGGTCACAGACATGTCTTCTCATCAGGAGGAAG 50
|||||
1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17
51 CCCCCCTGTAAAGCATCTCCAGATGAGGGGATGAGCCCATGCCGATCC 100
|||||
17 rProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCGAGGACCTCTCCACACCTCGGGAGGACAGCAAGCTCCCAAGAGTAC 150
|||||
34 rGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGTAGAGAA 200
|||
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
201 TGGCGGTGCTGTGAATGATGGGGAAGATGTGCGGAGGATTTACGAA 250
|||||
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
251 TGTCTGTATGCTCGGGAGAGAAAATGAATGGCTCCACAGGAGCAAGGC 300
|||||
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301 AGCTCGGCTTTGTGCGGAGTTGGAGGATTCGACTTCCTAACGGAAACT 350
|||||
101 SerSerAlaLeuSerGlyValGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCAT 400
|||||
117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
401 TTCACAAAAGAGCCACACTGGAGAACGGCCCTTCCAGTGCATACAGTGC 450
|||||
134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer 150

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451 GGGGCTCATTCACCCAGAGAGGCAACCTGCTCCGGCACATCAAGCTGCA 500
|||||
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
|||||
501 TTCGGGGAGAGCCCTCAATATGCACTCTGCAACTACGCTGCCGCC 550
|||||
167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArg 184
|||||
551 GGAGGAGCCCTCACTGCGCACCTGAGGACGCACTCGTGGTAAACCT 600
|||||
184 rArgAspAlaLeuThrGlyHisLeuArgThrHisSer..... 196
|||||
601 CACAAATGTGATATTGTGGCGAAGCTATAAACACGCGAAGCTCTTTAGA 650
196 ..... 196
651 GGAACATAAAGAGCGCTGCCACAACACTTGTGAAAGCATGGCCCTTCGG 700
196 ..... 196
701 GCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAATGGCA 750
196 ..... 196
751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTGCTGGACAGACT 800
196 ..... 196
801 AGCAAGTATGTGCCCAACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
197 .....G 197
851 GGGACAAGGCGCTTCGCACAGCCCTACGACAGTCCACGTACGAGAAG 900
|||||
197 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 213
||| :|||
901 GAGAACAATATGATGAATGCCACGTGATGGACCAAGCCATCAACAACGC 950
||| :|||
214 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAl 229
|||||
951 CATCAACTACCTGGGGCGGAGTCCCTGCGCCCGCTGGTGGACAGCCGCC 1000
|||||
229 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 246
|||||
1001 CGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC 1050
|||||
246 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 262
||| :|||
1051 AGG...CGTCTGGAGGCGACCCCGCTCCAAAGTTCGCTCCGCTCCG 1097
||| :|||
263 LysProProSerAspGlyProArgProArgSerAsnHisSerAlaGlnAsp.. 278
|||||
1098 CGCGGTGGAGTACTGCTGCTCTCCAAAGTTCGCTCCGCTCCGCTCCG 1147
||| :|||
279 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 295
|||||
1148 AGCGGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGACACCGGAG 1197
|||||
295 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 311
|||||
1198 AGCAACAACGAGGAGGAGCGCGCTCTTACTCTGCTGCTGCTGCTGCT 1247
|||||
312 SerAsnAlaGluGluArgSerGlyLeuIleTyrLeuThrAsnHisIl 328
|||||
1248 CGCCCGGCGCGCAAGCC...GTGCTGCTCAAGGAGGAGGAGGAGGAG 1294
||| :|||
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|||||
1295 ACGACCTGCTCGCGCGCGCTCCGAGAACTCGCAGGAGGAGGAGGAGG 1344
||| :|||
345 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 361
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